

# All Documentation on Wiki

SJTU-Software

2014.10

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# 1 HOME

## EASY BBK

An EASY Biobrick Blueprint's packAge

Difficulties in finding biobricks in need and in interpreting bio-systems presented in different styles remain to be two main problems in synthetic biology. Our team has created "Easy BBK" to help users get neat information and evaluation of specific biobricks quickly and to display their bio-system easily. Users can input keywords of the biobrick they are interested in, and select special requirements of certain properties, and related biobricks will be searched, sorted and displayed. Ascore will be computed for each biobrick, based on the current status, reliability, feedbacks of users, number of publication and etc. Additionally, users could draw their bio-system easily with the standardized biobrick icons, and they can also look into the detailed information about the biobricks in the bio-system. Finally, new biobricks can be uploaded directly and automatically to Registry of Standard Biological Parts through our 'Easy BBK' system.

## 2 SOFTWARE

### 2.1 Overview

EASY BBK: An EASY Biobrick Blueprint's packAge

We have constructed an Easy Biobrick Blueprint's packAge (EASY BBK) to assist users to search biobricks of good quality, compare the quality of biobricks, present bio-systems with standardized icons and upload biobricks to Registry or Easy BBK database.

#### Search

This function enables users to search by keywords or by sequence against our database. Advanced search mode is also provided to refine or sort the search results. In default mode, search results are sorted by a score given by our assessment model.

The searching engine is based on a database converted from the iGEM Registry (Up to 2014 August). More details on database: <http://2014.igem.org/Team:SJTU-Software/Database>.

#### Compare

Multiple biobricks can be added from search engine and then compared. You can search and get multiple (up to three) biobricks, and compare them side by side.

#### Present

In this function, a standardized picture of a biosystem could be plotted with standardized biobrick icons according to the iGEM Registry. The result can be exported, which could be used for the presentation in the publication, presentation or later design. Additionally, with presented biobricks connected with database, the upload form could be directly filled out in "upload".

#### Upload

Here, users could not only upload their biobricks to our database, but also submit their form filled out in our software to the Registry to upload their self-created biobricks.

## 2.2 Tutorial

“Easy BBK(An Easy Biobrick Blueprint’s packAge)” has four main function: “search”, “compare”, “present”, and “upload”. This part will guide users about how to use this software tool.

### 2.2.1 How to start EASY BBK

Software environment: Java SE Development Kit 6 and later version.

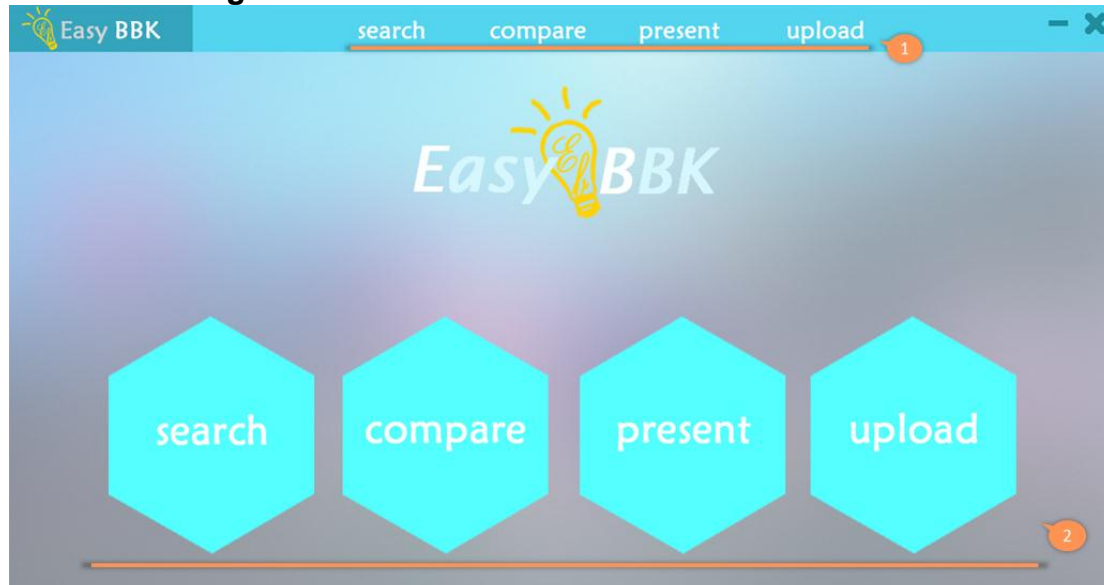
1. Download EASY BBK from github
2. Download the latest JDK from

<http://www.oracle.com/technetwork/java/javase/downloads/index.html>

Java SE Development Kit 8u25		
You must accept the <a href="#">Oracle Binary Code License Agreement for Java SE</a> to download this software.		
<input type="radio"/> Accept License Agreement <input checked="" type="radio"/> Decline License Agreement		
Product / File Description	File Size	Download
Linux x86	135.24 MB	<a href="#">jdk-8u25-linux-i586.rpm</a>
Linux x86	154.88 MB	<a href="#">jdk-8u25-linux-i586.tar.gz</a>
Linux x64	135.6 MB	<a href="#">jdk-8u25-linux-x64.rpm</a>
Linux x64	153.42 MB	<a href="#">jdk-8u25-linux-x64.tar.gz</a>
Mac OS X x64	209.13 MB	<a href="#">jdk-8u25-macosx-x64.dmg</a>
Solaris SPARC 64-bit (SVR4 package)	137.01 MB	<a href="#">jdk-8u25-solaris-sparcv9.tar.Z</a>
Solaris SPARC 64-bit	97.14 MB	<a href="#">jdk-8u25-solaris-sparcv9.tar.gz</a>
Solaris x64 (SVR4 package)	137.11 MB	<a href="#">jdk-8u25-solaris-x64.tar.Z</a>
Solaris x64	94.24 MB	<a href="#">jdk-8u25-solaris-x64.tar.gz</a>
Windows x86	157.26 MB	<a href="#">jdk-8u25-windows-i586.exe</a>
Windows x64	169.62 MB	<a href="#">jdk-8u25-windows-x64.exe</a>

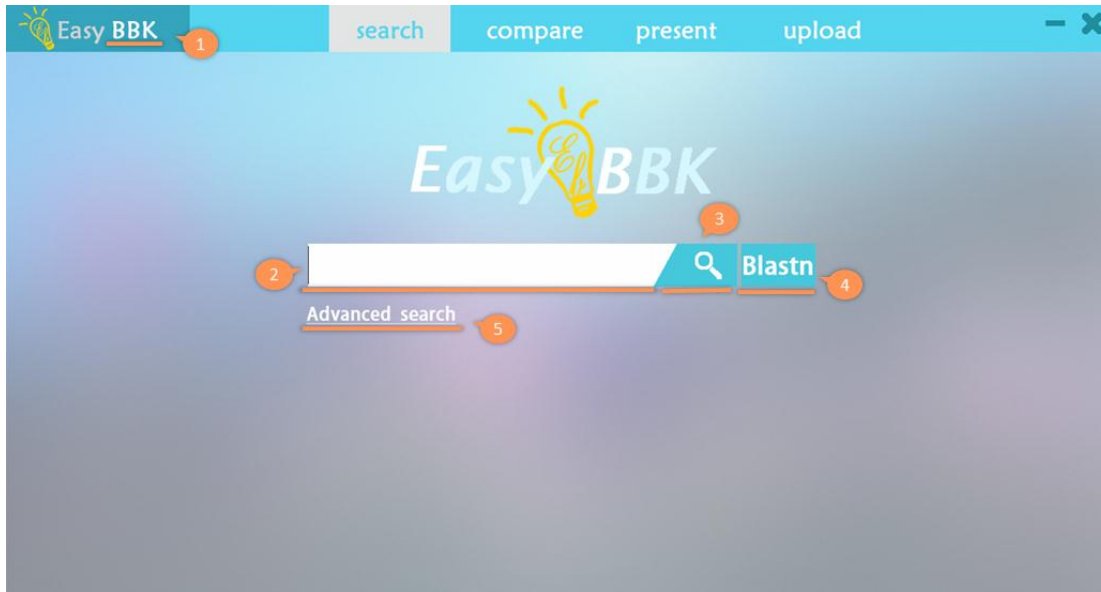
3. Double click the Easybbk.jar and start Easybbk

### 2.2.2 Home Page

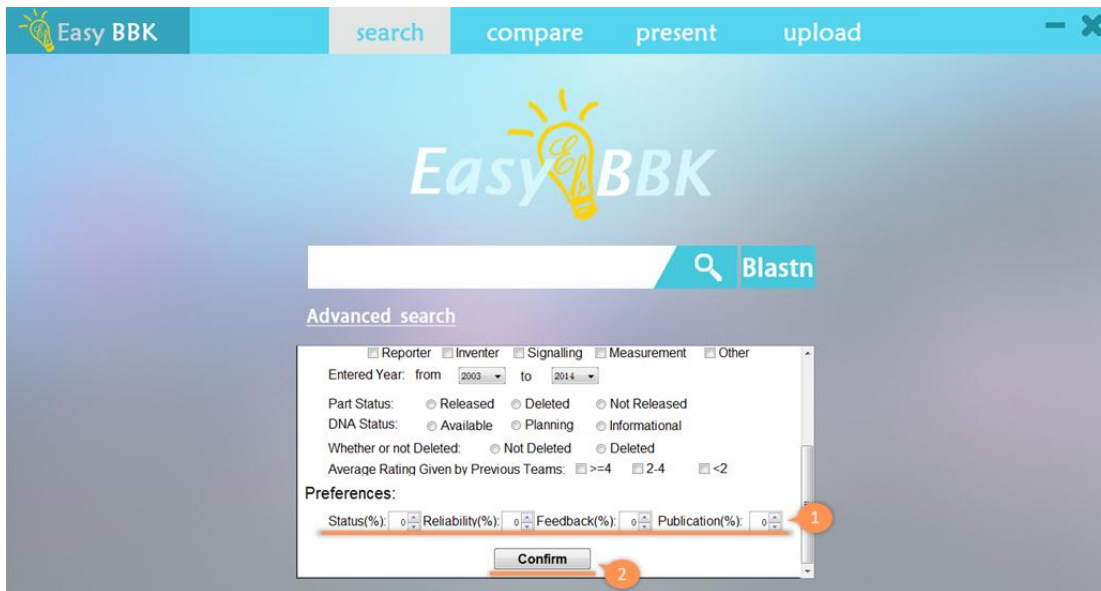


1/2. Click each icon to enter each function

### 2.2.3 Search



1. Go back to home page
2. Input keyword or sequence
3. Search by keyword
4. Search by sequence
5. Display advanced search conditions



1. Adjust the weight of the 4 properties to make them add up to 100
2. Click "Confirm" before starting search by keyword or sequence

**BBa\_J23114** Type: Regulatory 69.86  
 Entered Date: 2006/8/17 Used Times: 40  
 Short Description: constitutive promoter family member  
 Author: John Anderson  
 Main Page of This Part: [http://parts.igem.org/Part:BBa\\_J23114](http://parts.igem.org/Part:BBa_J23114)  
 Part Status: Released HQ 2013 Average Rating: 5  
 Number of Related Results on Google Scholar: 8

**BBa\_J23113** Type: Regulatory 69.21  
 Entered Date: 2006/8/17 Used Times: 37  
 Short Description: constitutive promoter family member  
 Author: John Anderson  
 Main Page of This Part: [http://parts.igem.org/Part:BBa\\_J23113](http://parts.igem.org/Part:BBa_J23113)  
 Part Status: Released HQ 2013 Average Rating: 5  
 Number of Related Results on Google Scholar: 12

**BBa\_J23118** Type: Regulatory 69.16  
 Entered Date: 2006/8/17 Used Times: 54  
 Short Description: constitutive promoter family member  
 Author: John Anderson  
 Main Page of This Part: [http://parts.igem.org/Part:BBa\\_J23118](http://parts.igem.org/Part:BBa_J23118)

[<previous page](#) 2 [next page>](#) total: 359

**BBa\_R0040**  
 Type: Regulatory  
 Entered Date: 2003/1/31  
 Author: " June Rhee, Connie Tao, Ty Thomson, Louis Waldman"  
 Short Description: TetR repressible promoter

Sequences:  
 tcctcatcagtgatagagattgacatccctatcagtgatagagatactgagcac

Main Page on Registry:  
[http://parts.igem.org/Part:BBa\\_R0040](http://parts.igem.org/Part:BBa_R0040)  
 URL of the most related publication:  
[https://openwetware.org/images/0/08/BreakItDown\\_Tech\\_Spec\\_Powerpoint.pdf](https://openwetware.org/images/0/08/BreakItDown_Tech_Spec_Powerpoint.pdf)

**Status**  
 Part Status: Released HQ 2013  
 Sample Status: In stock  
 DNA Status: Available  
 Delete this Part: Not Deleted  
 Confirmed Times: 5  
 Length of Documentation: 31610

**Reliability**

1. Forward or Back to previous or next page
2. Display detail information of the biobrick
3. Click to view the main page of the biobrick on iGEM Registry
4. Check to add the biobrick to "compare"
5. Click to view the result most related to the biobrick on Google Scholar
6. Go to the previous page of search results
7. Go to the next page of search results
8. After biobricks being added from "search", click to go to "compare" the biobricks

## 2.2.4 Compare

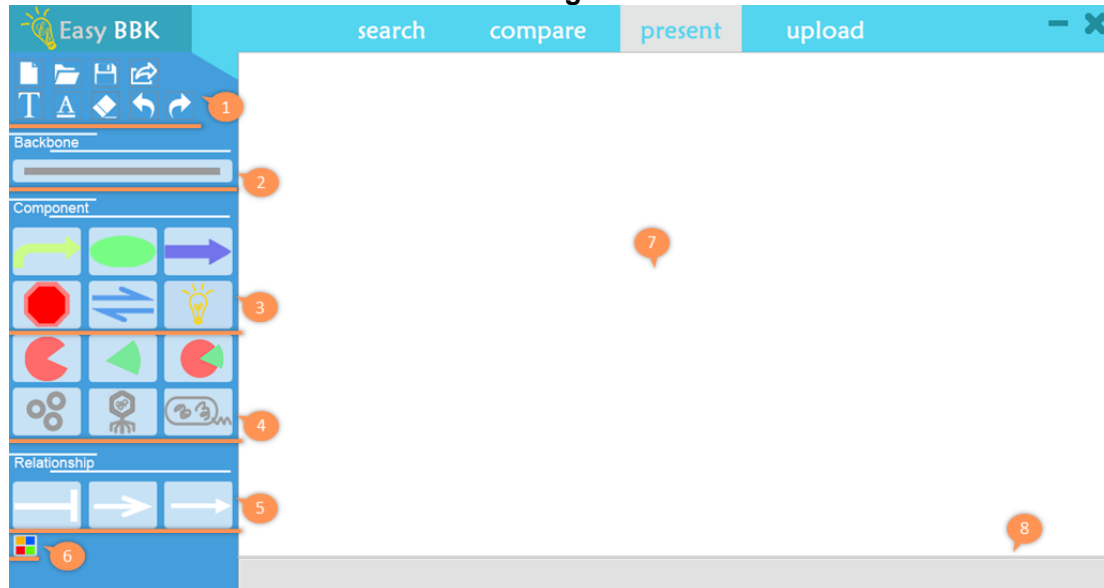
**The Comparison for Biobricks**

	<b>BBa_R0040</b>	<b>BBa_J23103</b>
<b>Part Name</b>	BBa_R0040	BBa_J23103
<b>Type</b>	Regulatory	Regulatory
<b>URL</b>	<a href="http://parts.igem.org/Part:BBa_R0040">http://parts.igem.org/Part:BBa_R0040</a>	<a href="http://parts.igem.org/Part:BBa_J23103">http://parts.igem.org/Part:BBa_J23103</a>
<b>Short Description</b>	TetR repressible promoter	constitutive promoter family member
<b>Status</b>		
Part Status	Released HQ 2013	Released HQ 2013
Sample Status	In stock	In stock
DNA Status	Available	Available
Delete this Part	Not Deleted	Not Deleted
Confirmed Times	5	3
Length of Documentation	31610	33272
<b>Reliability</b>		
Part Results	Works	Works

1. Remove the biobrick below from "Compare"
2. Click to view the main page of the biobrick on iGEM Registry
3. After biobricks being viewed in "compare", click to go back to "search" results

## 2.2.5 Present

### 2.2.5.1 General introduction of Present Page



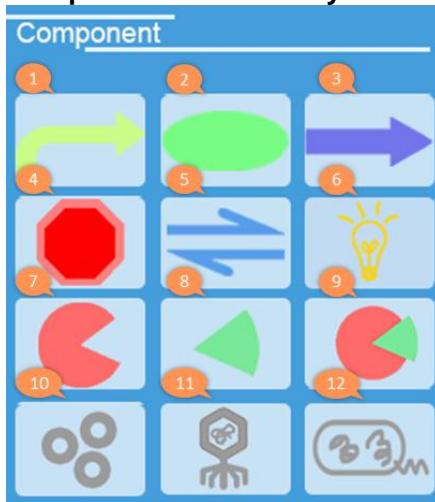
1. Basic Functions
2. Backbone
3. Components on backbone
4. Proteins, plasmid, virus and bacteria
5. Relation between biobricks
6. Style settings of lines above
7. Bio-system drawing panel
8. Status bar

#### Basic Functions



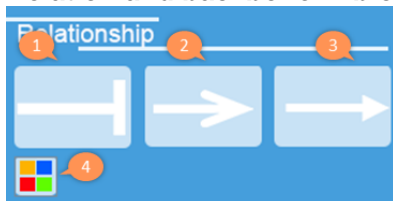
1. Discard previous work and create a new bio-system
2. Open previously saved XML file
3. Save the drawn bio-system as an XML file to further edit next time
4. Export the picture of the bio-system as .jpg, .bmp or .png file.
5. Add text to the drawing panel
6. Change the font, size and color of the text
7. Delete components on drawing panel
8. Undo
9. Redo

## Components on in bio-systems



1. Promoter
2. Ribosome binding site (RBS)
3. Protein coding sequence
4. Terminator
5. Primer
6. Reporter
7. Protein 1
8. Protein 2
9. Combined protein
10. Plasmid
11. Virus
12. Bacteria

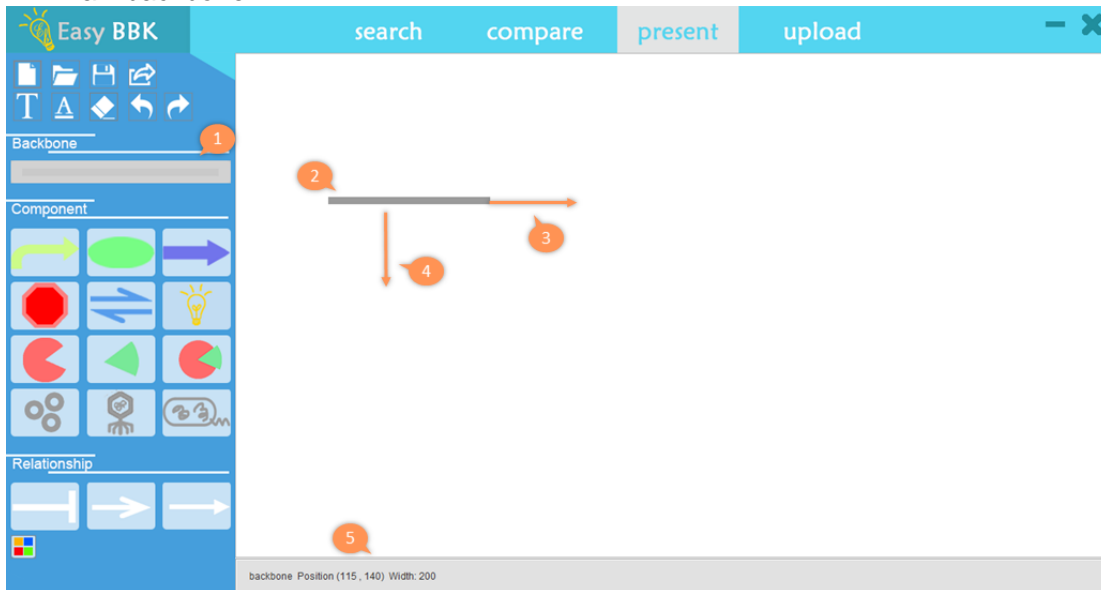
## Relation and backbone in bio-systems



1. Inhibit
2. Enhance
3. Other relations (e.g. this could denote a coding sequence code a protein.)
4. Backbone
5. Style settings of lines above

### 2.2.5.2 Start presenting your bio-system

1<sup>st</sup>: Draw backbone



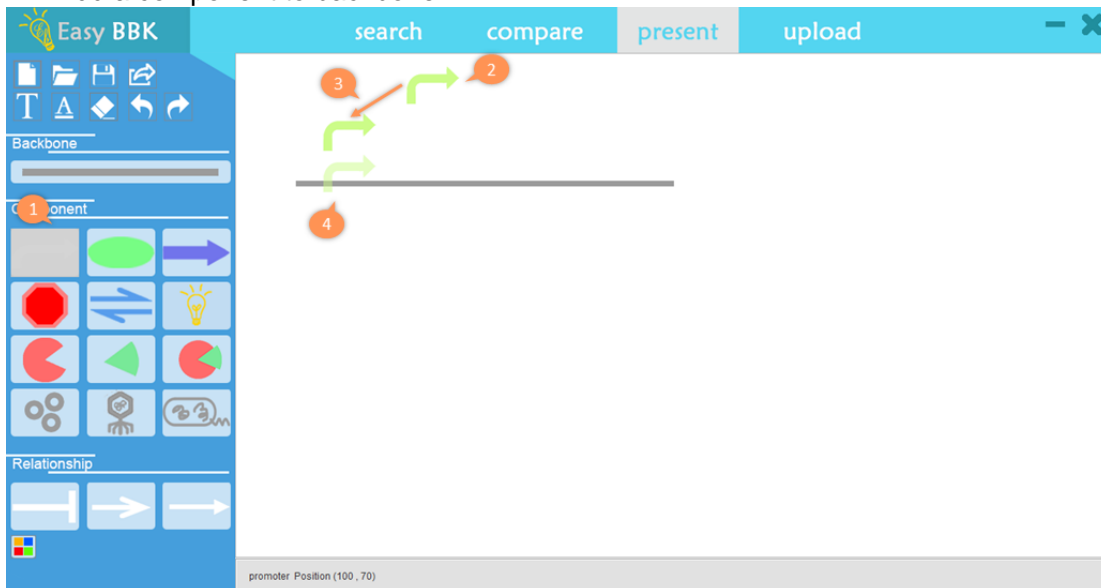
Step 1. Click the “Backbone” icon

Step 2. Click anywhere on drawing panel to add a “Backbone”

Step 3. Stretch the “Backbone”

Step 4. Drag the “Backbone” to anywhere on drawing panel

2<sup>nd</sup>: Add a component to backbone



Step 1. Click the “Promoter” icon

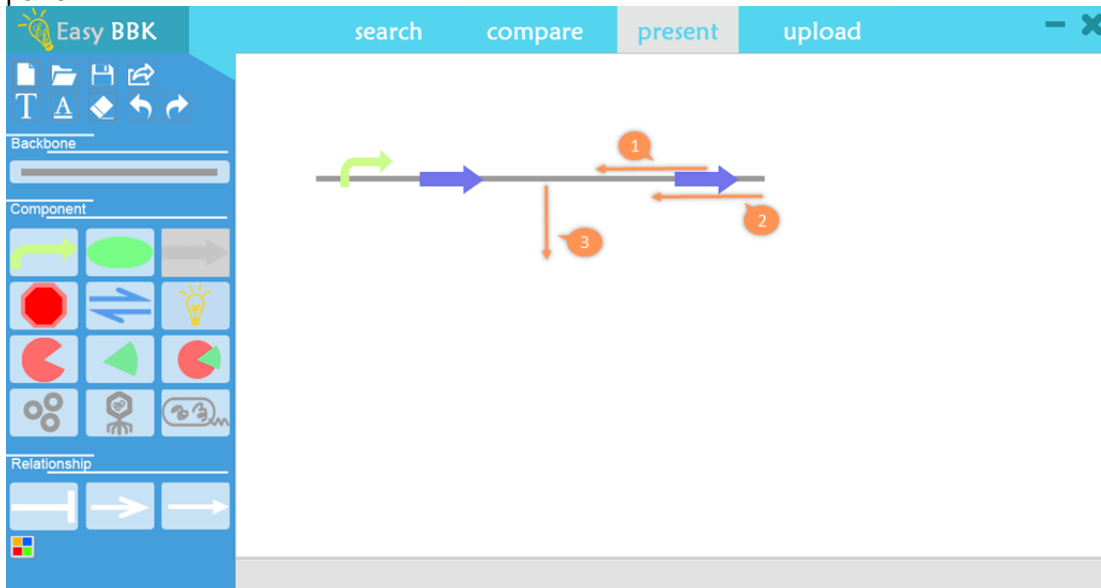
Step 2. Click anywhere on drawing panel to add a “Promoter”

Step 3. Drag the “Promoter” near “Backbone”

Step 4. Release the mouse to make the “Promoter” automatically become part of the sequence

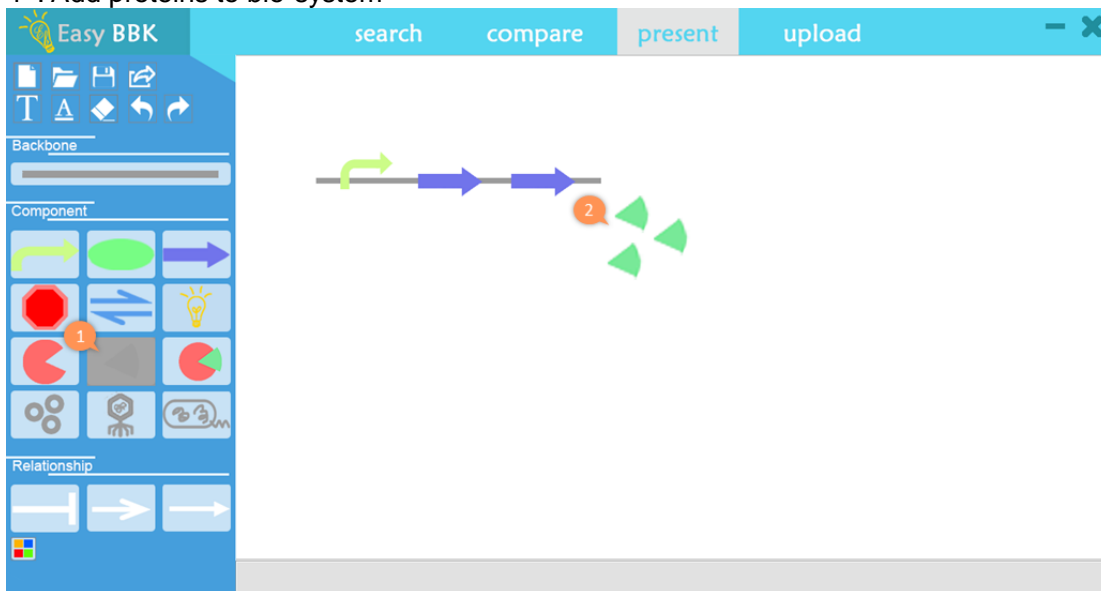


3<sup>rd</sup>: Adjust the position of the components or backbones already existing on the drawing panel



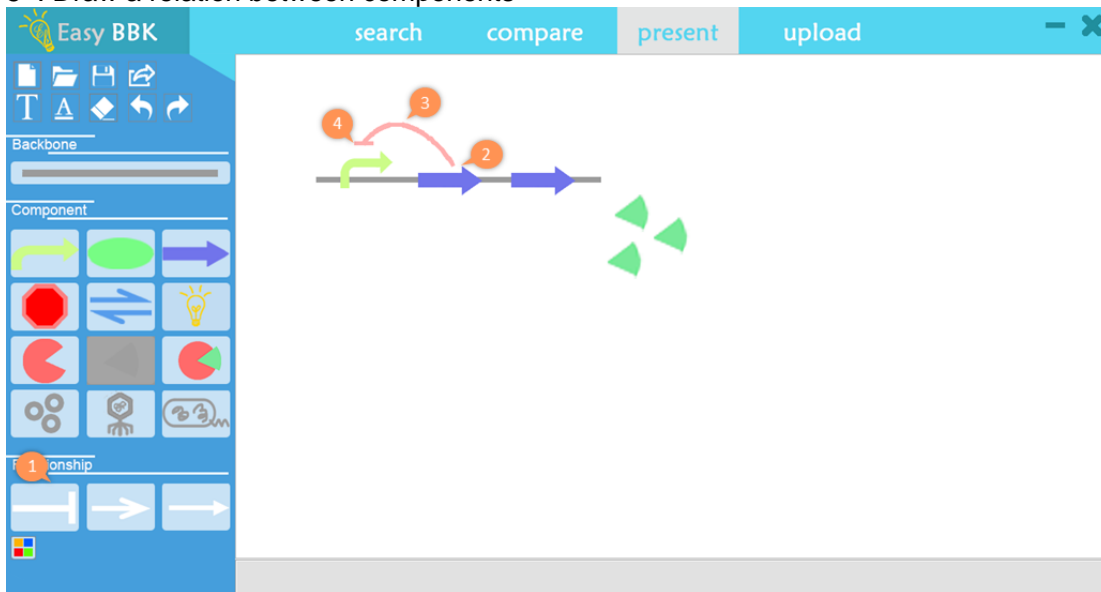
1. Drag the “Protein Coding Sequence” to a suitable position
2. Stretch the “Backbone” to a suitable length
3. Drag the “Backbone” to anywhere on drawing panel

4<sup>th</sup>: Add proteins to bio-system



- Step 1. Click the “Protein 2” icon
- Step 2. Click anywhere on drawing panel to add proteins

5<sup>th</sup>: Draw a relation between components



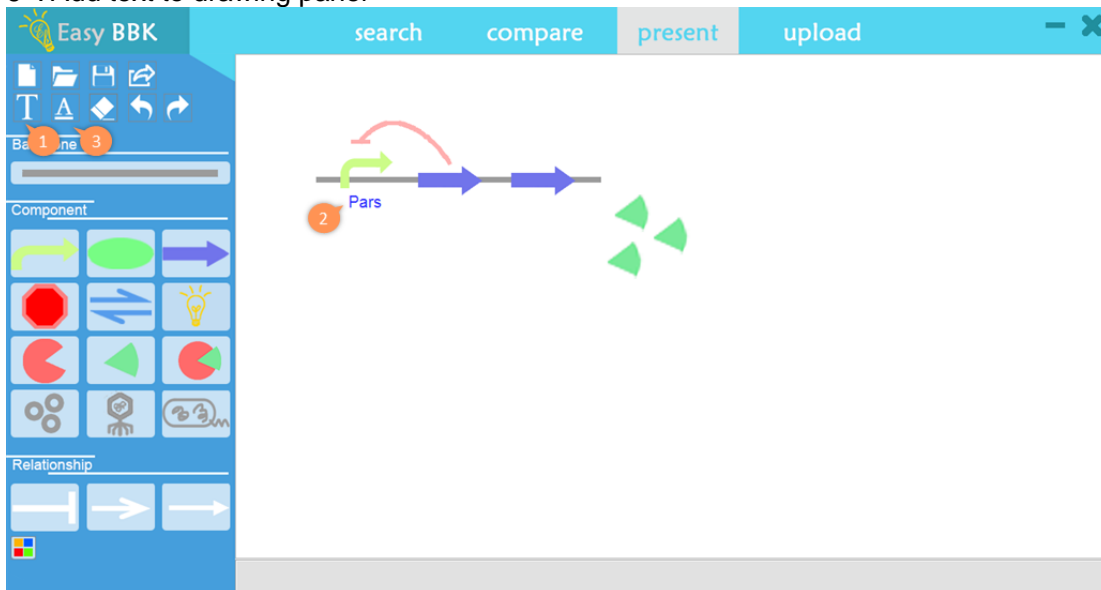
Step 1. Click the “Inhibit” icon

Step 2. Click here

Step 3. Click here

Step 4. Click here (More clicks could be done until you get your desired shape of this relation.)

6<sup>th</sup>: Add text to drawing panel

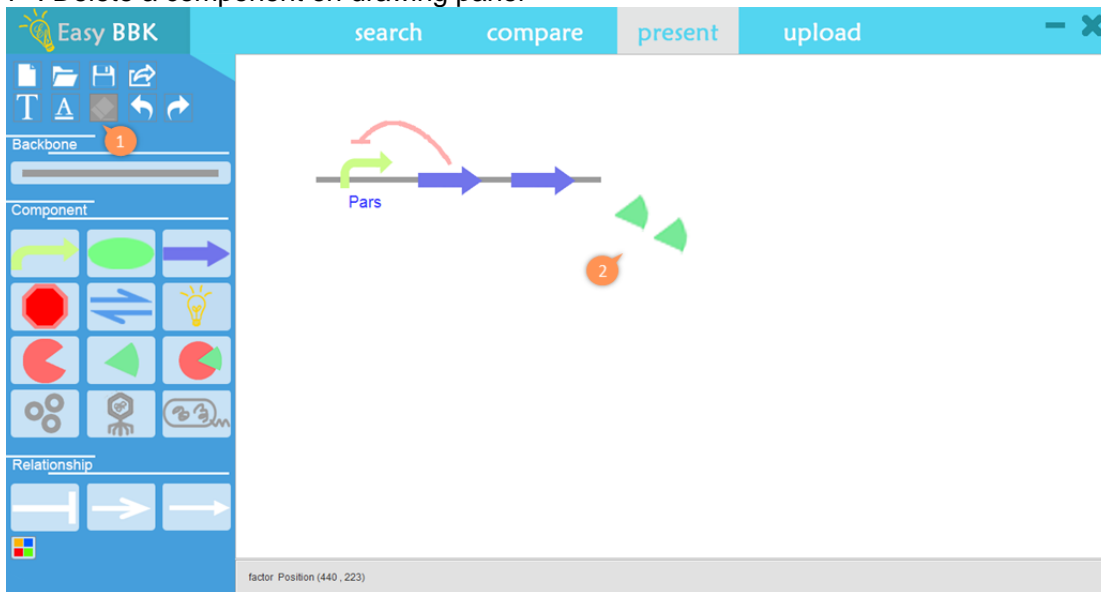


Step 1. Click the “Text” icon

Step 2. Click anywhere on drawing panel to add text

Step 3. Click to change the font, size and color of the text

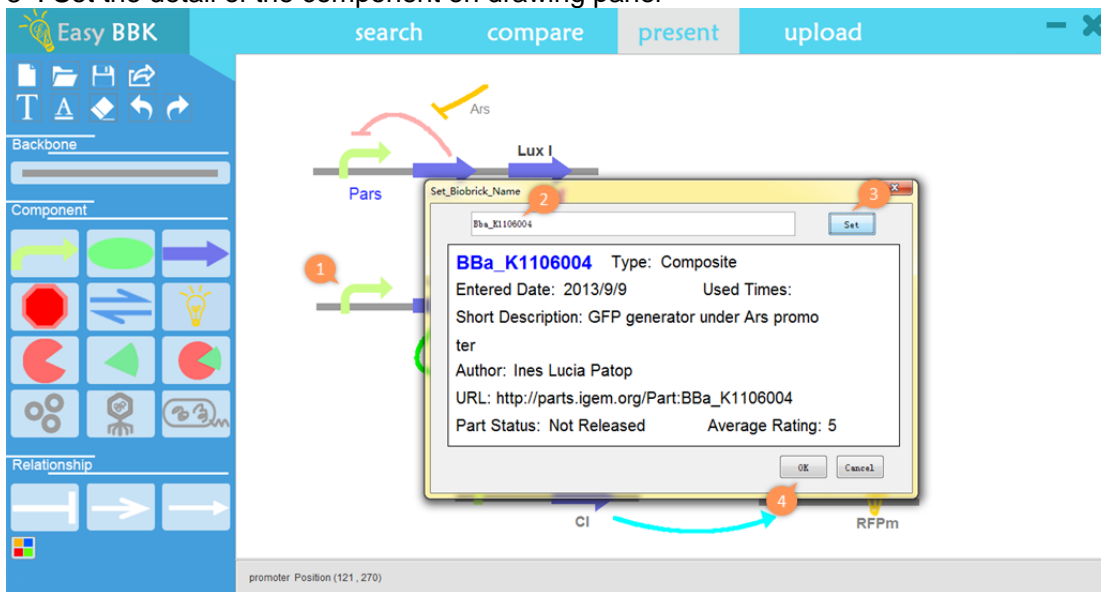
7<sup>th</sup>: Delete a component on drawing panel



Step 1. Click this icon

Step 2. Click any component on drawing panel to delete it

8<sup>th</sup>: Set the detail of the component on drawing panel



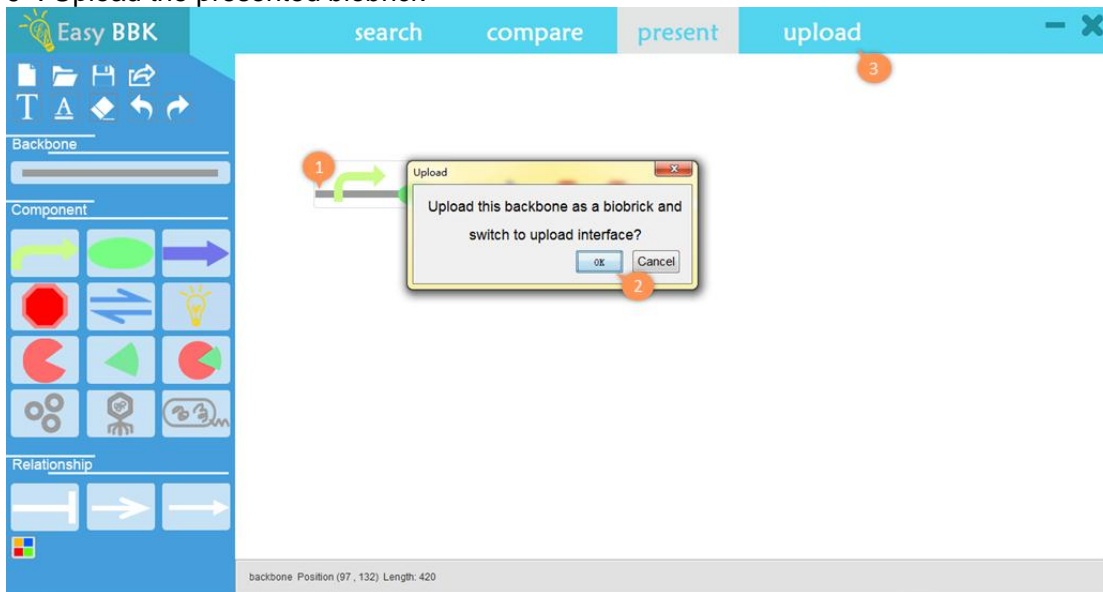
Step 1. Double click any component on backbone

Step 2. Input a part name

Step 3. Click "Set" to search this part out from database

Step 4. Click "OK" to set the detail of the component

9<sup>th</sup>: Upload the presented biobrick



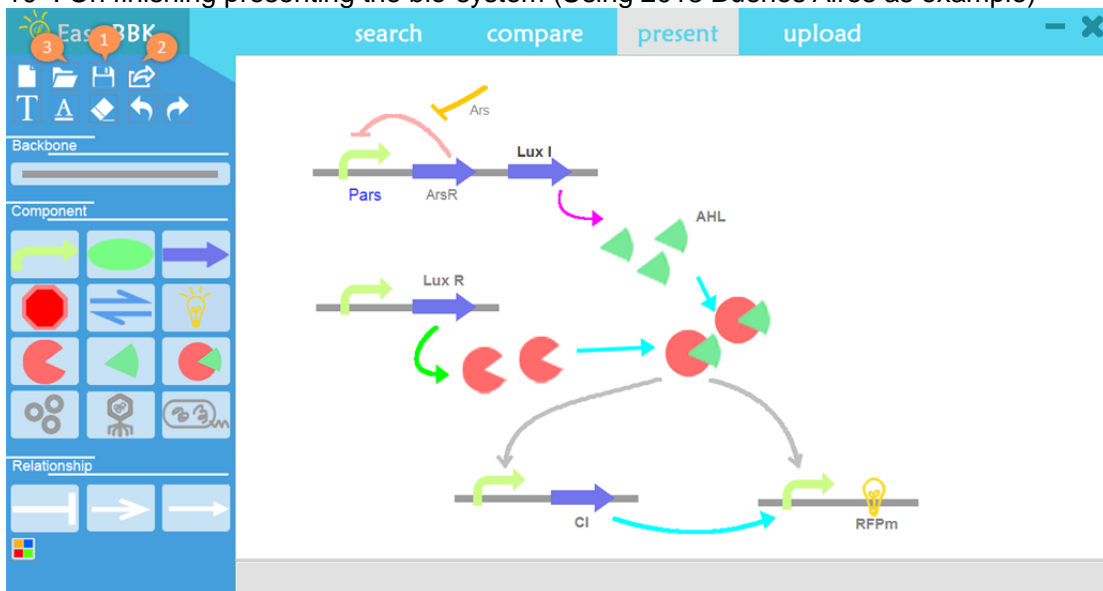
By setting the detail on all the biobricks on a single backbone, user can choose to upload the biobrick to Registry or Easy BBK database. The upload form will be automatically filled out.

Step 1. Double click the backbone of the biobrick

Step 2. Click “OK” to confirm to upload the biobrick

Step 3. Go to “upload” to check the filled out form

10<sup>th</sup>: On finishing presenting the bio-system (Using 2013 Buenos Aires as example)



Step 1. Save the drawn bio-system as an XML file to further edit next time

Step 2. Export the picture of the bio-system as .jpg, .bmp or .png file.

Step 3. Open previously saved XML file continue drawing

## 2.2.6 Upload

Easy BBK search compare present upload

Welcome to the Upload Page! Clear All

1 A short description of this biobrick:

Type: Promoter

Nickname:

Designer(s):

Sequence Information:

Add sequence Add subpart Add subscar

☒ Use default scar

Parameters: Add Remove

1. Input information of biobrick

Easy BBK search compare present upload

Bba\_K1106000.

part so that users of your part know what it is, what it does, and how to use it in their projects.

Contents below only can be uploaded to Registry!

The source of this part:

Design Consideration:

Enter the source of this part. For example, does it come from some genomic sequence?

Enter any design considerations you had to deal with during the detailed design of the sequence.

IGEM Username: Password: 1

Submit to EasyBBK Submit to Registry 2 3

1. Input iGEM user name and password
2. Click to submit the biobrick to Easy BBK database
3. Click to submit the biobrick to Registry

## 2.3 User Study

### 2.3.1 Goal

User studies are carried out to make our software “Easy BBK” to be more user-friendly. Based on the problems exposed in the test process of different users and their feedbacks, our developers can track the bugs and add new functions in the development of software.

### 2.3.2 Users

9 members from SJTU-bioX-Shanghai and some members from SUSTC-Shenzhen were

invited to use our software. All of their operations are recorded in video and researched later to figure out problems or highlights in our software.

### 2.3.3 Highlights and problems fixed

Since we have focused mainly on the problems in our software during those studies, highlights are briefly recorded here.

- The search result offered by the search engine are quite satisfying
- Novelty of “Present”

Most problems identified during user studies were solved before wiki freezes; however, there remains some problems unsolved. Those problems which are not solved now are to be solved later, and we will continue conducting user studies to refine our software.

Problems solved by October 17<sup>th</sup>

Problem	Solution	Solved date
User doesn't know detail information of a biobrick could be displayed	Distinguish the color of part name from other information	10.12
Spelling errors exist in some words on the interface	Make corrections on these mistakes	10.12
The detail page was not refreshed timely when user clicked another part name to view the detail of this part	Revise the source code to make the detail page refresh timely	10.12
User wants to know the number of search results	Revise the source code to show the number of search results at the bottom of the page	10.12
User don't know the meaning of the icons on the “present” interface	Add a new function: a text description about an icon would come out when user moves cursor to it	10.12
Half-drawn bio-system lost when user accidentally clicked the “create a new file” button	A dialog box asking user whether to save the half-drawn bio-system would pop up when user click the “create a new file” button	10.12
User didn't know what to do with the “compare” function	Add a hint on the interface to guide the user	10.13
User cannot remove a biobrick from compare to add another biobrick after adding it to compare	Add a button to remove biobricks from “compare”	10.13
The text disappeared after user changed the font or color of the text in “Present”	Revise the source code to solve this bug	10.13
The software would export a wrong picture if user had dragged components out of the screen	Revise the source code to solve this bug	10.13
The hint on the search result page was confusing when there is no search result	Revise the English expression on the result page	10.13
User misunderstood the meaning of the “cross” button in “present” for its inappropriate position	Adjust the position of different buttons	10.17

Run time of the search engine is unstable	Create index on tables in Easy BBK database and change the database to a better server to speed up run time	10.15
The status bar of “present” cannot automatically refresh unless user clicked the same position once more	Revise the source code to solve this bug	10.15
The icon of “Blast” on the “search” interface confused users in that they thought it could do “blastp”	Change the icon from “Blast” to “Blastn”	10.15
Icon positions of “search by keyword” and “search by sequence” were too close to mislead user that they have a single function	Increase the distance between the two icons	10.15
On the status bar, the coordinate of the icon became negative when the icon was dragged out of the drawing panel, which is meaningless	Set the coordinate of deleted icon to “NULL”	10.16
The icons in “present” interface was too vague	Refresh the icon with high-resolution pictures	10.16
User did not know how to fill out the “upload” page	Add some examples beside the input boxes	10.16

Problems remained unsolved and under development until October 17<sup>th</sup>

Problems	Planning solution	Planning date
User did not know they can stretch the backbone	Put anchors on both end of the backbone to hint users	10.19
User didn't know the function of “set_biobrick_name” window	Add the hint “input part name” beside the input field	10.19
User cannot copy text from the search result page and paste in other functions in the tool	Revise the source code to solve this problem	10.20

## 2.4 Demo

This demo guides you to the function “search” and “compare”:

This demo guides you to the function “present” and “upload”:

If you want more detailed information, please click this link for user tutorial:  
<http://2014.igem.org/Team:SJTU-Software/Project/Tutorial>

## 2.5 Download

Different versions for different platforms can be downloaded here:

[https://github.com/igemsoftware/SJTU-Software\\_2014](https://github.com/igemsoftware/SJTU-Software_2014)

Complete list of documentations on this wiki can be downloaded here:

# 3 DOCUMENT

## 3.1 Database

Here, we have reconstructed the database of the current existing biobricks. All the necessary information available on the Registry are collected and used to construct our own database.

In this part, the source of data, the way of data collection, database structure and some facts of the biobricks in the database are introduced.

### 3.1.1 Data collection

Data are collected from 5 different websites on the Registry and Google Scholar. The data needed in the reconstructed biobrick database is available from 5 sources, with four of them from the websites of Registry of Standard Biological Parts and 1 of them from Google Scholar. Addresses of those sources for BBa\_B0034 are listed in Table 2.1.1, and the part name could be replaced by any biobrick.

Name of Websites	Address
XML format	<a href="http://parts.igem.org/cgi/xml/part.cgi?part=BBa_B0034">http://parts.igem.org/cgi/xml/part.cgi?part=BBa_B0034</a>
Hard information	<a href="http://parts.igem.org/cgi/partsdB/part_info.cgi?part_name=BBa_B0034">http://parts.igem.org/cgi/partsdB/part_info.cgi?part_name=BBa_B0034</a>
Get part	<a href="http://parts.igem.org/partsdB/get_part.cgi?part=BBa_B0034">http://parts.igem.org/partsdB/get_part.cgi?part=BBa_B0034</a>
Experience	<a href="http://parts.igem.org/Part:BBa_B0034:Experience">http://parts.igem.org/Part:BBa_B0034:Experience</a>
Google scholar	<a href="http://scholar.google.com.cn/scholar?q=BBa_B0034">http://scholar.google.com.cn/scholar?q=BBa_B0034</a>

**Table 3.1.1** Sources of the data in the biobrick database, using BBa\_B0034 as an example

PERL scripts are composed to connect to those links and to pick out the information we need. In order to connect to those links, we need to understand the way how biobricks on the website are named. There exist two main ways to name the biobricks, which are illustrated in Table 2.1.2 and Table 2.1.3. “BBa” is used for most biobricks, names of which consist of 3 parts. The first part is “BBa\_”; the second part is a capitalized letter; the third part is several digits, the number of which depends on the previous capitalized letter (possible combinations are listed in Table 2.1.2). “pSB” is specially used for plasmids, names of which consist of 4 parts. The first part is “pSB”; the second part is one digit ranging from 1 to 9; the third part is a single pattern or a combination of two patterns listed; the fourth part can be any number from 1 to 29.

The First Part of the Name	The Second Part of the Name	The Third Part of the Name (Number of Digits)	Examples
BBa_	A	6	BBa_A340620
	B	4	BBa_B0034
	C	4/5/6	BBa_C0053; BBa_C10001;
	E	4	BBa_E5504
	F	4	BBa_F2622
	G	4/5	BBa_G0011; BBa_G00500
	I	4/5/6	BBa_I10018;
	J	4/5/6	BBa_J52100; BBa_J540013
	K	6/7	BBa_K374013; BBa_K1218016
	M	4/5	BBa_M1904; BBa_M31000
	P	4	BBa_P2007
	Q	5/6	BBa_Q200514
	R	4	BBa_R4037
	S	5	BBa_S01297



	T	4	BBa_T1009
	V	4	BBa_V1022
	Y	5	BBa_Y00100
	Z	4/5	BBa_Z0506; BBa_Z52935

**Table 3.1.2** Rules in naming biobricks starting with “BBa\_”

The First Part of the Name	The Second Part of the Name	The Third Part of the Name	The Fourth Part of the Name	Examples
pSB	1~9	A/C/E/G/K/N/N a/R/S/St/T/Tm/ Z	1~29	pSB1K16
pSB	1~9	Combination of 2 letters above	1~29	pSB4AC5

**Table 3.1.3** Rules in naming biobricks starting with “pSB”

By substituting the names listed in Table 2.1.2 and Table 2.1.3 for the part name (BBa\_B0034) in the addresses listed in Table 2.1.1, we can get access to the links about the information on biobricks. Data that are collected by PERL scripts from each website are listed in Table 2.1.4. More detailed description of those data are available in Table 2.1.5. PERL scripts used to collect those data are available on GitHub.

Name of Websites	Address
XML format	part id; part name; part short name; part short description; part type; part status; sample status; part results; part nickname; part rating; part url; part entered; part author; Sequences; Samples; References; groups; deep subparts; specified subparts; specified subscars; features; parameters; categories; twins;
Hard information	DNA status; Group Favorite; Whether or not deleted; Used Times; Length of Documentation
Get part	Confirmed Times; Not Confirmed Details
Experience	Average Rating; Number of Comments
Google scholar	Number of Publication; URL of the most related publication

**Table 3.1.4** Data collected from the 5 sources

Property	Description
part id	ID of the part in Registry
part name	Official name of the part
part short name	Part name without “BBa_”
part short description	The short description is usually a biological or technical descriptor of the part. It will show up on the part page
part type	This will state the part type/function, and will show up at the top of the part page, to the left of the DNA Status
part status	The status of the part based on the completeness of its documentation and characterization.system not currently in place
sample status	The status of the part's physical DNA (sample) in the Repository
part results	The experience status for a part, as documented by the part authors

part nickname	Nickname of the part
part rating	Whether there is a registry star for the part
part url	URL of main page for the part
part entered	Entered date of the part
part author	Author of the part
Sequences	Nucleotide sequence of the part
Samples	It's not enabled now
References	It's not enabled now
Groups	It's not enabled now
deep subparts	All subparts that compose the subparts in the part
specified subparts	All subparts that compose the part
specified subscars	All scars between subparts
Features	Features of the part
Parameters	The parameters are submitter-decided, allowing for a degree of technical specification for the part.
Categories	Categories allow for a part to become content in automatically generated part tables, which is important in defining the organization of your part within the Registry, and specifically for the Catalog of Parts and Device
Twins	Two or more parts are twins if they have the same sequence
DNA status	States the DNA status of your part: Deleted, Planning, Sent, Available, etc. These statuses are generated by the Registry, so the user cannot edit them.
Group Favorite	One can choose if the part is a favorite of your team/group.
Whether or not deleted	Whether the part is deleted
Used Times	The number of times the part has been specified in composite parts in the Registry
Confirmed Times	The number of times the part sequence has been confirmed by users
Not Confirmed Details	Details of not confirmed facts
Average rating	The mean value of rating for the part given by users
Number of Comments	The number of comments from users
Number of Publication	The number of related results of the part on Google Scholar
URL of the most related publication	The most related result of the part on Google Scholar

### 3.1.2 Database Structure

The structure of the database is presented in Figure 3.1. The primary key in table “Main” is “part name”, with all the other tables linked to it by identical “part name”. There is no primary key in the tables except “Main” because biobricks could belong to more than one category or have more than one twins. Thus, the part name in the rest tables could be repeated for several times, depending on different biobricks.

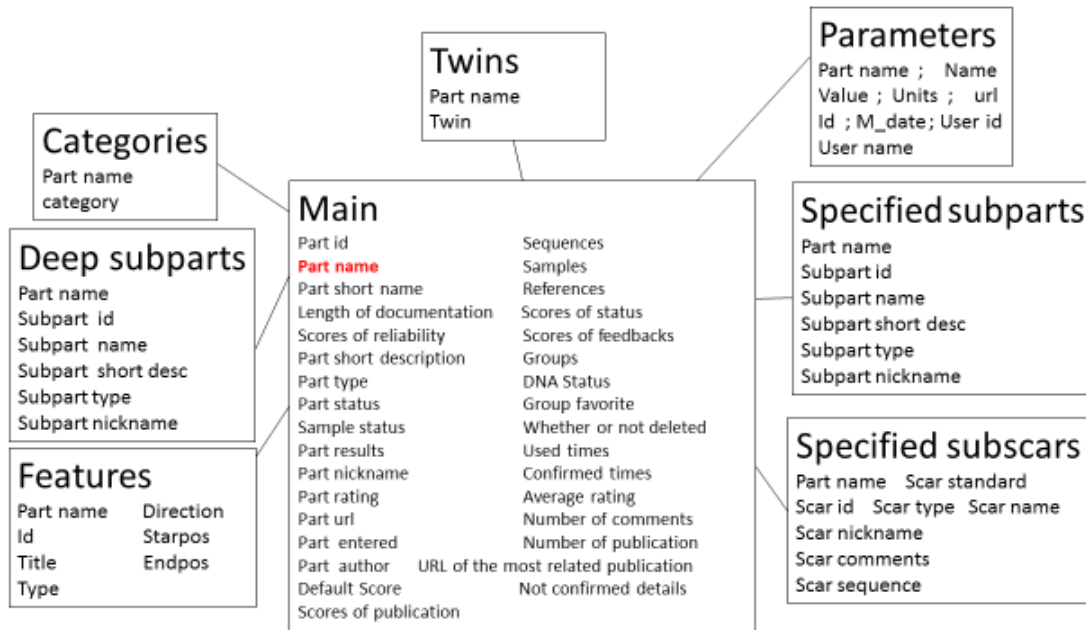
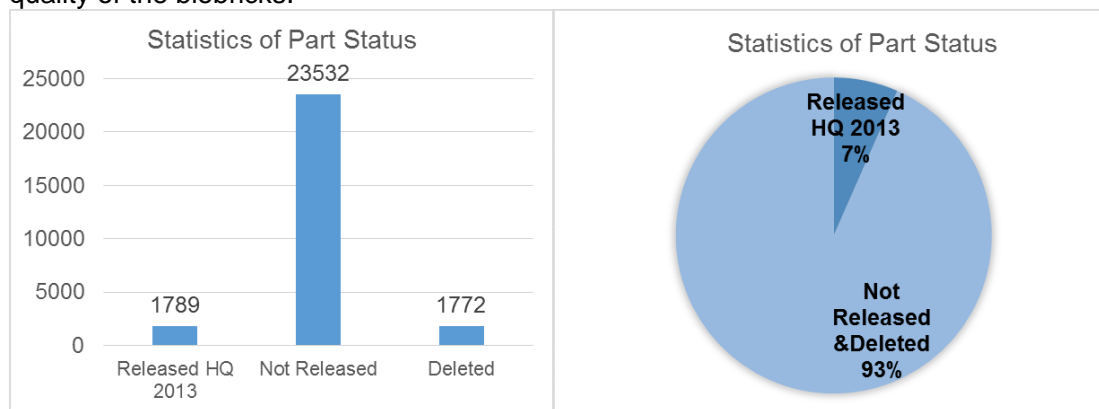
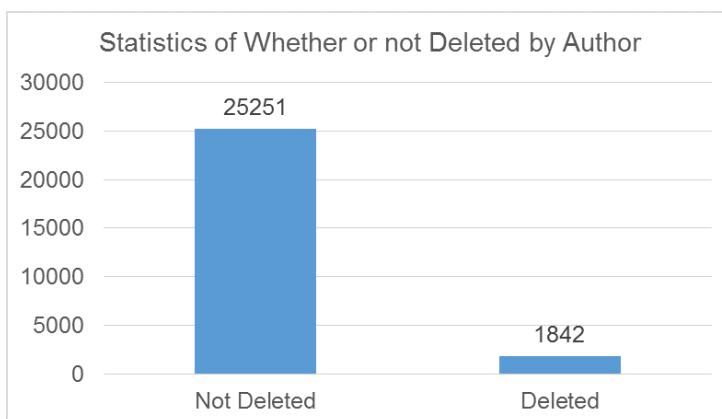
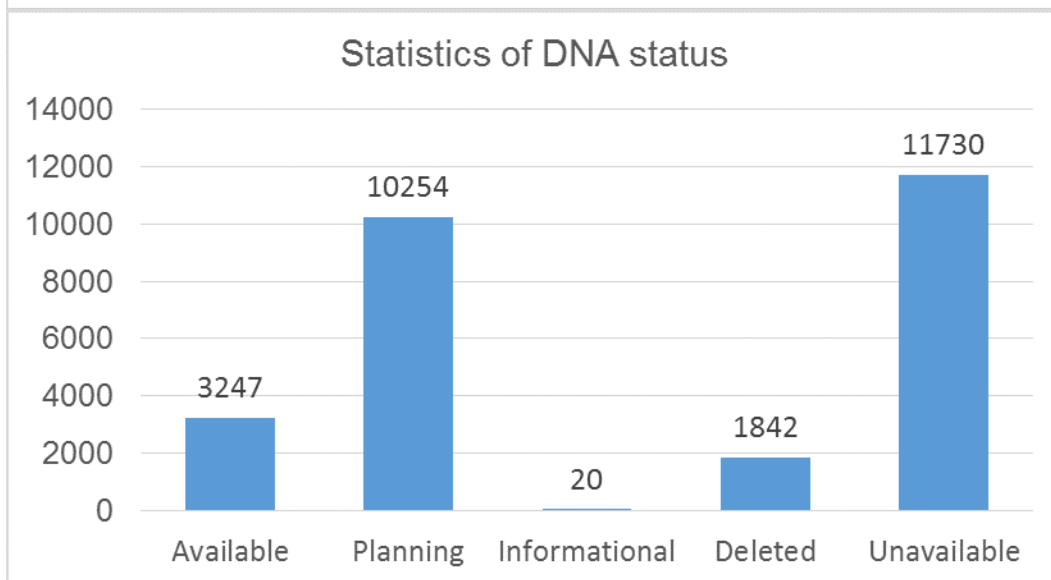
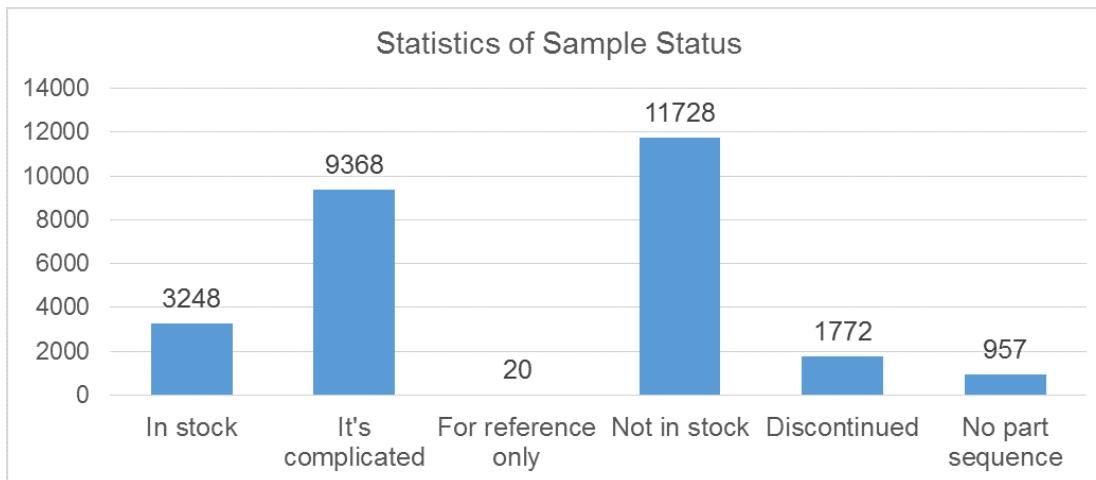


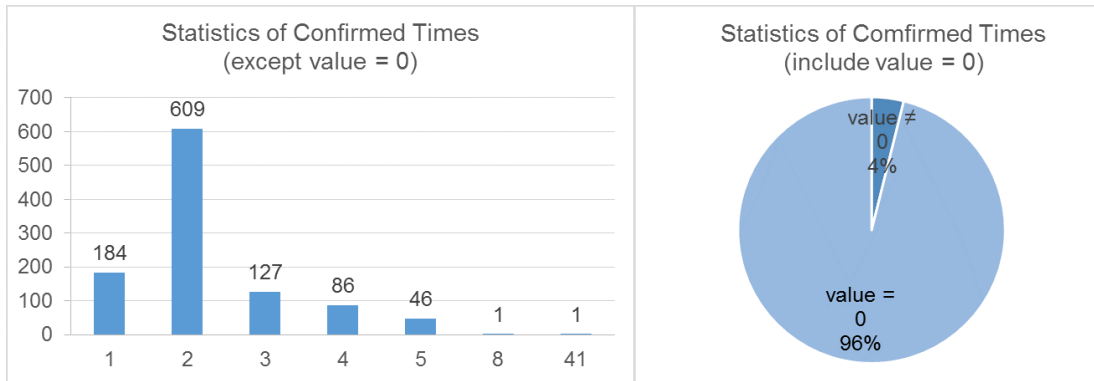
Figure 3.1 The structure of the reconstructed biobrick database

### 3.1.3 Quick Facts about the Biobricks

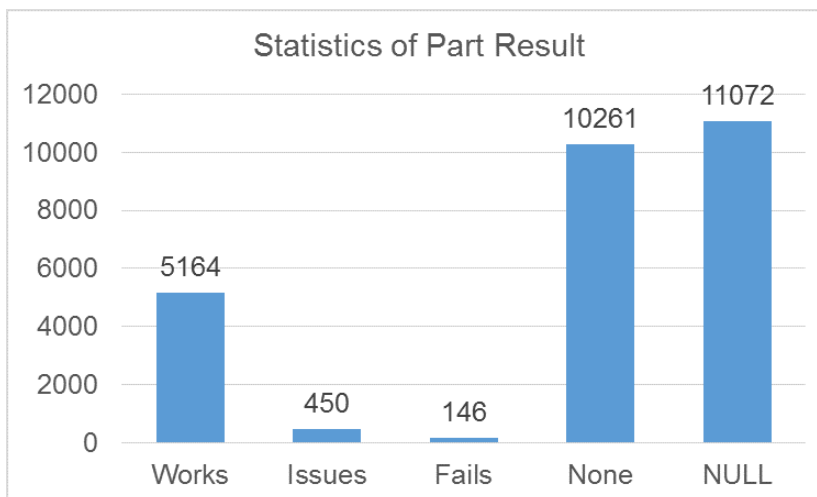
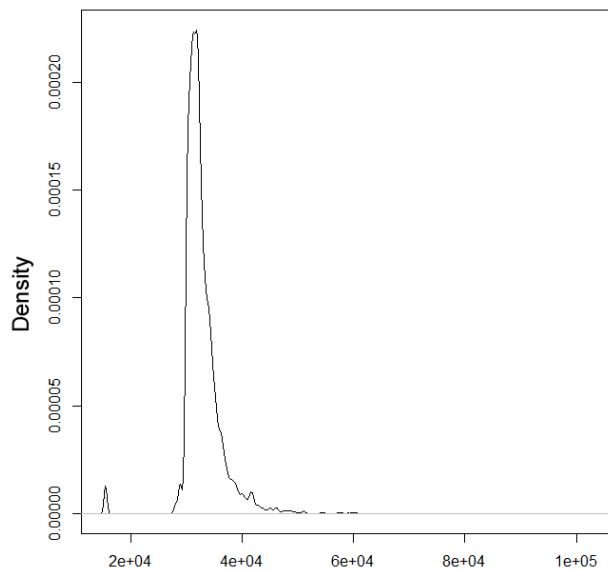
Here are figures counting the number of the values of some important attributes judging the quality of the biobricks.

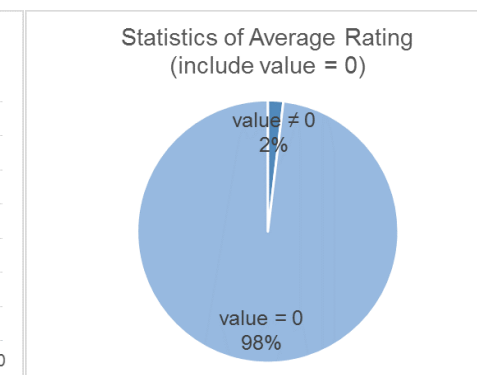
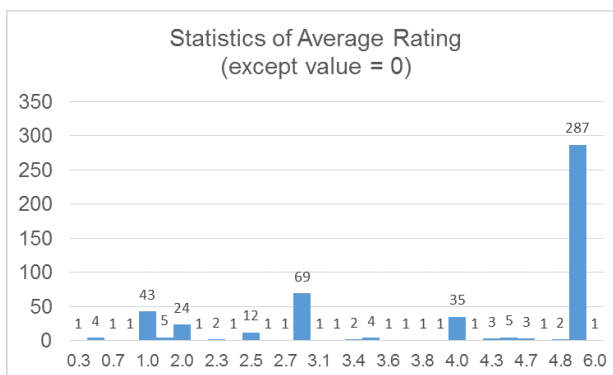
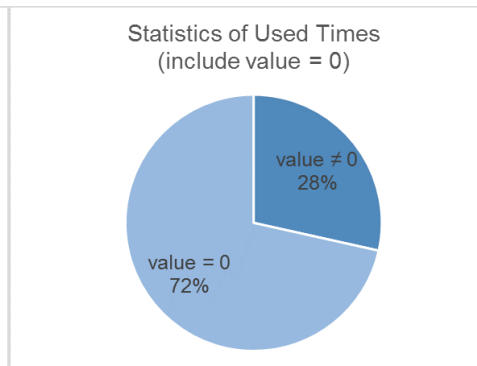
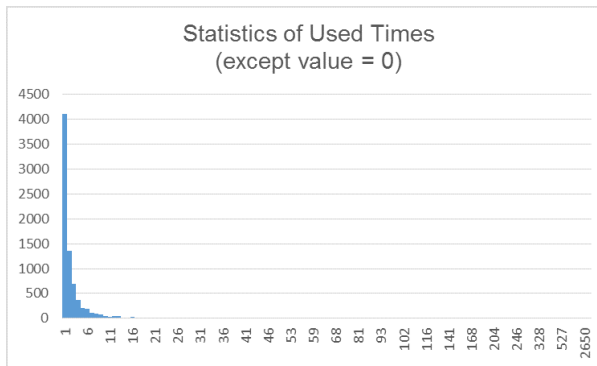
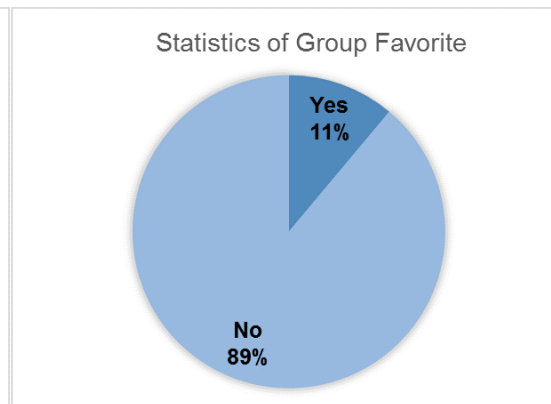
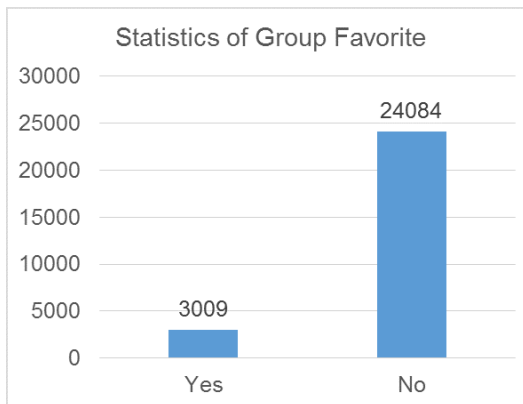
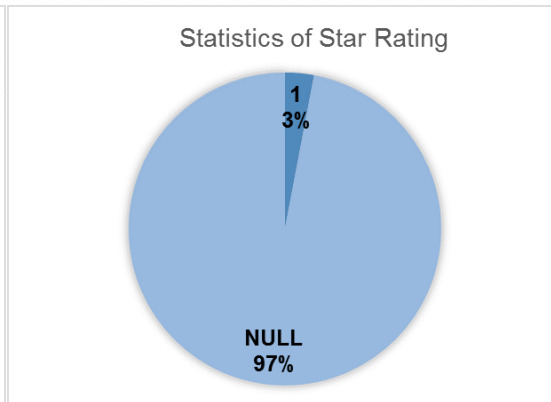
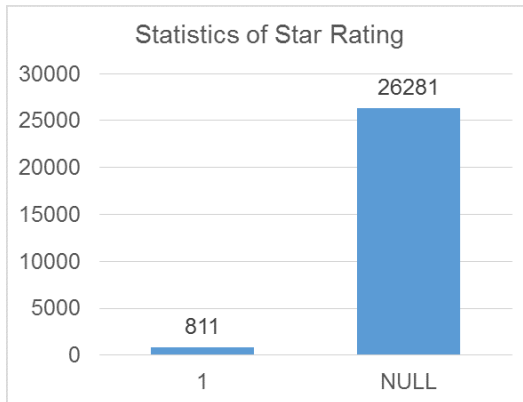


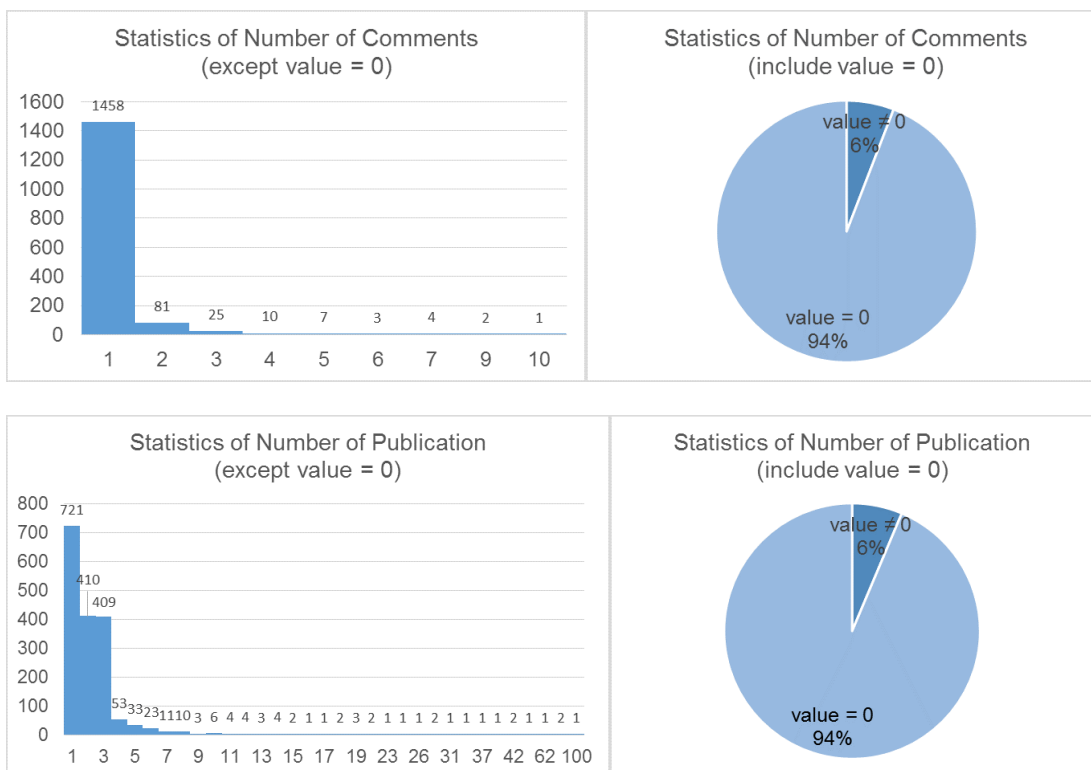




Statistics of Length of Documentation







## 3.2 Assessment Model

An assessment model is optimized to judge the quality of biobricks. With a default score given to each biobrick respectively, biobricks that are related to the input keyword in the “Easy BBK” search engine can be listed in descending order of scores although users can define their own sorting order. If sorted by default scores, users can always get biobricks with high quality. Our assessment model considered 4 general properties, namely status, reliability, feedback and publication, based on 12 attributes of a biobrick. Weights of the attributes in the general properties are already optimized and fixed; weights of the 4 general properties can be adjusted by users although default weights of the properties are optimized already and recommended to users.

### 3.2.1 Evaluation criteria

Based on the description on the website of Registry of Standard Biological Parts and advice collected from our instructor, 13 attributes of biobricks are picked out as evaluation criteria in the assessment model.

Considering different aspects users frequently takes into account when choosing a biobrick, we deliberately divided these attributes into 4 properties, which are listed in Table 3.2.1.

Property	Description
Status	Will I get this official part? This property measures the availability of the part.
Reliability	Will this part work? This property measures the working quality of the part.
Feedback	What is the review of previous teams or experimenters for this part?

	This property collects the feedbacks of previous workers on the part.
Publication	How many publications are related to this part? This property contains the related results on Google Scholar.

Table 3.2.1 The four properties in the assessment model

More detailed description of the attributes in the properties are demonstrated in Table 3.2.2.

Property	Attribute	Description
Status	Part Status	The status of a part based on the completeness of its documentation and characterization.
	Sample Status	The status of the part's physical DNA (sample) in the Repository.
	DNA Status	States the DNA status of your part: Deleted, Planning, Sent, Available, etc. These statuses are generated by the Registry, so the user cannot edit them.
	Whether or not Deleted	Whether the part is deleted or not.
	Confirmed Times	Times of the sequence of the part being confirmed. Part samples are sequenced using the VF2 and VR primer sites on their plasmid backbones. Sequence results are then uploaded and compared to their target sequence (part's documented sequence) through Registry software.
	Length of Documentation	Length of documentation for the part on Registry
Reliability	Part Results	The experience status for a part, as documented by the part authors. However, the part's experience is not a validation of the part by iGEM HQ.
	Star Rating	Stars given by Registry
	Group Favorite	Whether the part is a favorite of one team/group.
Feedback	Used Times	The number of times the part has been specified in composite parts in the Registry.
	Average Rating	The average rating given for this part by other users.
	Number of Comments	Times being reviewed by other users)
Publication	Number of Publication	Number of related literatures and webpages on Google scholar

Table 3.2.2 Detailed attributes in the assessment model

### 3.2.2 Scores given to the values in each criterion

There are two types of values in all the criteria: categorical variables (such as part status, part results, etc) and continuous variables (such as used times, average stars, etc).

For categorical variables, we give reasonable scores to different values in each criterion based on the researchers' experience and description of the values.



For continuous variables, we normalize the values in those criteria using the following formula, so that all the continuous variables range from 0 to 1 like categorical variables:

$$x' = \frac{x - \min(x)}{\max(x) - \min(x)}$$

where  $x$  is an original value,  $x'$  is the normalized value.

The scores given to different values in all the attributes is presented in Table 3.2.3.

Attribute	Status	Score	Number
Part Status	Released HQ 2013	1	1789
	Deleted; Not Released	0	25304
Sample Status	In Stock	1	3238
	It's complicated	0.5	9368
	For Reference Only	0.25	20
	Not In Stock; No Part Sequence; Discontinued	0	14457
DNA Status	Available	1	3247
	Planning; Informational	0.5	10274
	Unavailable; Deleted	0	13572
Whether or Not Deleted	Not Deleted	1	25251
	Deleted	0	1842
Confirmed Times	Normalized values ranging from 0 to 1		27093
Length of Documentation	Normalized values ranging from 0 to 1		27093
Part Results	Works	1	5164
	Issues	0.5	450
	Fails; None; NULL	0	21479
Star Rating	1	1	811
	NULL	0	26282
Group Favorite	Yes	1	3009
	No	0	24084
Used Times	Normalized values ranging from 0 to 1		27093
Average Rating	Normalized values ranging from 0 to 1		27093
Number of Comments	Normalized values ranging from 0 to 1		27093
Number of Publication	Normalized values ranging from 0 to 1		27093

Table 3.2.3 Different scores given to the different values in all the criteria

### 3.2.3 Weights given to each criterion

50 biobricks were picked out as positive samples in Table 3.2.4. The weight of each criterion are then trained and adjusted to make the biobricks in the positive samples ranking the highest in the final scores.

Positive Examples	Type	Reasons of choosing these parts as positive samples
BBa_B0034	RBS	These two parts were most frequently used and well rated. BBa_B0034 is the RBS used most and BBa_B0015 is the terminator used most.
BBa_B0015	Terminator	
BBa_E1010 BBa_E0040	Coding Region	These two parts are well documented and they perform well in other attributes.
BBa_J23114 BBa_J23113	Regulatory	These two parts are not outstanding in any attribute, however, they are better than most of the other parts in all of attributes.
BBa_R0040 BBa_R0010	Promoter	These two parts are used most frequently among promoters and they get good feedbacks from users

Table 3.2.4 Part of the positive samples in our assessment model

The weights of the criteria in each property are fixed and cannot be adjusted by users. In “Easy BBK”, users could adjust the weight of the 4 properties - Status, Reliability, Feedback, Publication - in our assessment model although optimized weights and default scores have already given to the biobricks in the assessment model. The optimized weights are presented in Table 3.2.5.

Property	Attribute	Default Weight	Weight
Status	Part Status	40.6%	1.6%
	Sample status		6.9%
	DNA status		8.3%
	Whether or not deleted		6.6%
	Confirmed times		11.4%
	Length of Documentation		5.8%
Reliability	Part results	23.3%	11.9%
	Star rating		10.2%
	Group favorite		1.2%
Feedback	Used times	24.4%	11.3%
	Average Rating		2.2%
	Number of comments		10.9%
Publication	Number of publication	11.7%	11.7%

Table 3.2.5 Weights given to the attributes in the default score of the biobricks

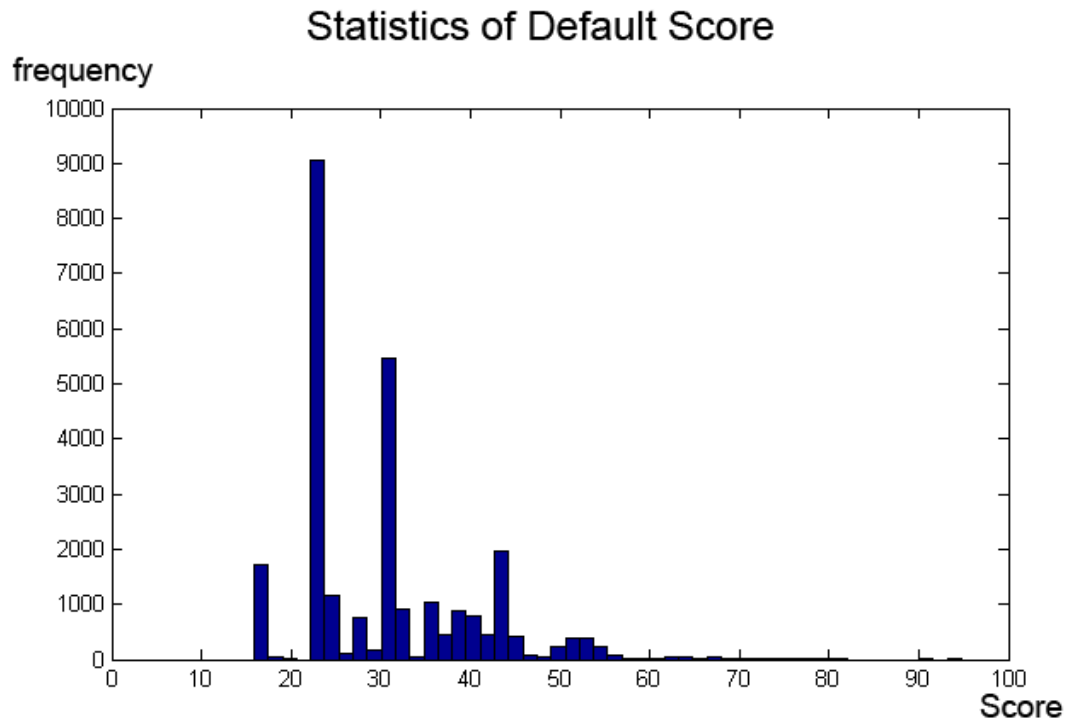
### 3.2.4 A glance at the assessment results

Table 3.2.6 shows the first three biobricks of different types:

Type	Biobrick	General information
<b>Coding</b>	BBa_E1010	Commented 7 times with average rating 3.14, 264 uses in composite parts, 23 records on Google Scholar
	BBa_E0040	Commented 5 times with average rating 3, 435 uses in composite parts, 32 records on Google scholar
	BBa_I712019	Commented 4 times with average rating 4
<b>Composite</b>	BBa_K081022	1 registry star, group favorite, commented one time with average rating 5
	BBa_K145279	1 registry star, group favorite, commented one time with average rating 5
	BBa_K137055	1 registry star, group favorite, 2 records on Google scholar
<b>RBS</b>	BBa_B0034	Commented 10 times with average rating 5, 2935 uses in composite parts, 62 records on Google scholar
	BBa_B0032	Commented 2 times with average rating 5, 487 uses in composite parts, 24 records on Google scholar
	BBa_B0030	Commented 3 times with average rating 4.33, 673 uses in composite parts, 9 records on Google scholar
<b>Regulatory</b>	BBa_R0040	Commented 7 times with average rating 4.14, 792 uses in composite parts, 31 records on Google scholar
	BBa_R0010	Commented 7 times with average rating 4.71, 549 uses in composite parts, 19 records on Google scholar
	BBa_R0011	Commented 9 times with average rating 3.44, 373 uses in composite parts, 13 records on Google scholar
<b>Reporter</b>	BBa_J04450	More documentation on website than others, commented 3



<b>Terminator</b>		times with average rating 5
	BBa_E0840	Group favorite, 138 uses in composite parts, 10 records on Google scholar
	BBa_J52008	Group favorite, Commented 3 times with average rating 5
	BBa_B0015	Commented 6 times with average rating 4.5, 2650 uses in composite parts, 70 records on Google scholar
	BBa_B0014	Commented 3 times with average rating 5, 248 uses in composite parts, 10 records on Google scholar
	BBa_B0011	76 uses in composite parts

The distribution of default scores of all biobricks is shown as follows:



BBa\_B0034 and BBa\_B0031 are both RBS, ranked the 1<sup>st</sup> and 4<sup>th</sup> in type RBS in our assessment model respectively. The information of the two biobricks is listed as follows.

	Part name	BBa_B0034	BBa_B0031
<b>Basic Information</b>	Short Description	RBS (Elowitz 1999) -- defines RBS efficiency	RBS.2 (weak) -- derivative of BBa_0030
	Part type	RBS	RBS
<b>Status</b>	DNA Status	Available	Available
	Release status	<u>Released HQ 2013</u>	<u>Released HQ 2013</u>
	Sample status	<u>Sample In stock</u>	<u>Sample In stock</u>
	Delete This Part	Not Deleted	Not Deleted
<b>Rating</b>	Qualitative Experience	Works	Works
	Group Favorite	No	No

	Star Rating	1	1
Feedback	Uses number	<u>2935 Uses</u>	<u>196 Uses</u>
	Comments number	10	2
	Comment stars		
Criterion	Number of Results in Google Scholar	62	28













Obviously, the two biobricks are the same in many attributes, and based on the overall information, we can generally conclude that the two parts are both of good quality.

However, when it comes to the number of used times, commented times, and number of results on Google scholar, it is suggested that BBa\_B0031 is less popular and has less number of studies than BBa\_B0034. What's more, on Registry, the definition of efficiency of BBa\_B0034 is 1.0, which is much higher than 0.07 of BBa\_B0031. This is also literally confirmed by their short description.

The conclusion above and our user studies have confirmed that the quality of biobricks is in accordance with the scores in our assessment model.

### 3.3 Components in present

Components in present was standardized using icons offered by Registry as standard.

Name	Registry	Easy BBK
Promoters		
Ribosome binding site		
Protein coding sequences		
Terminators		
Primers		
Reporters		

More components in present will be available in our next versions.

### 3.4 For Future Developers

Detailed API documentation automatically built from source code documentation using doxygen, documentation of automated unit testing and test coverage built using EclEmma and manual for perl script used for data collection can be downloaded [here](#).

### 3.5 Event in SJTU-Software

Time	Event
2013.12	Recruited Team members for 2014 iGEM in Shanghai Jiao Tong University (SJTU)
2014.1	Elected the team leaders of the wetlab, drylab and human practice
2014.2~2014.3	Researched the previous projects winning gold medals, especially software projects

2014.3	Made the decision to set up a software team in SJTU
2014.3~2014.4	Communicated our idea to the professors in our school and received approval to set up a software team
2014.4	Applied and registered our team at iGEM Headquarters
2014.4~2014.6	Judged final idea for the project
2014.7	Started working for the project
2014.8.3~2014.8.7	Four team members attended the Second iGEM Conference in National Chiao Tung University (NCTU)
2014.8.15~2014.8.17	Three team members attended meetup of software teams in China in University of Science and Technology of China (USTC)
2014.8.25	Code changed from C# to Java.
2014.9.10	"Easy BBK" database completed.
2014.9.25	The assessment model for biobricks completed.
2014.10.7	Release version 0.9.0 of Easy BBK

## 4 REQUIRMENT

### 4.1 Medal

Bronze. The following 4 goals must be achieved:

1. **Register the team, have a great summer, and have fun attending the Jamboree in Boston.**

We have registered a team named "SJTU – Software" in April. All of our team members have worked together and developed "Easy BBK" for the whole summer. Nine of our team members and one of our instructors will attend the Giant Jamboree in Boston this year at the beginning of November.

2. **Create and share a description of the team's project via the iGEM wiki.**

The address of our wiki is <http://2014.igem.org/Team:SJTU-Software/Overview>. The introduction, user tutorial and insight into our project is shared here.

3. **Present a Poster and Talk at the Regional Jamboree and World Championship Jamboree.**

We will talk and present a poster at the World Championship Jamboree.

4. **Develop and make available via The Registry of Software Tools, an open source software tool that supports Synthetic Biology based on Standard Parts.**

User could download Easy BBK here.

<http://2014.igem.org/Team:SJTU-Software/Project/Download>

Silver: In addition to the Bronze Medal requirements, the following 4 goals must be achieved:

1. **Demonstrate the relevance of your development for Synthetic Biology based on standard Parts.**

The assessment model in “Easy BBK” are based on the information of standard Parts collected from Registry. In the model, we have taken into consideration 13 attributes of the biobricks and have modified the weight of those attributes to rank the standard Parts in a reliable manner.

Additionally, the components in the “design” part of “Easy BBK” are based on the legend available on Registry. Although a little modification have been made on each component, they are easier to be identified by users.

**2. Provide a comprehensive and well-designed User Guide. (Be creative! An instructional video may work as well.)**

User Guide is available on this link:

<http://2014.igem.org/Team:SJTU-Software/Project/Tutorial>

**3. Provide detailed API documentation, preferably, automatically built from source code documentation (use tools like doxygen, yard, rdoc, naturaldocs, etc).**

Detailed API documentation are automatically built from source code documentation using doxygen. Download of this documentation is available through this link:

<http://2014.igem.org/Team:SJTU-Software/Database/FutureDevelopment>.

**4. Demonstrate that you followed best practises in software development so that other developers can modify, use and reuse your code. Provide more than one realistic test case. Examples of best practices are automated unit testing and documentation of test coverage , bug tracking facilities, documentation of releases and changes between releases.**

Documentation of automated unit testing, test coverage are built using EclEmma and are available through this link: .

<http://2014.igem.org/Team:SJTU-Software/Database/FutureDevelopment>. Bug tracking facilities, documentation of releases and changes between releases are available on Github.

Gold: In addition to the Bronze and Silver Medal requirements, two additional goals must be achieved:

**1. Provide a convincing validation, testing the performance of the development -- experimentally (can be outsourced) or by other teams and users. Note, even if the algorithm or tool turns out not to work that well, the Gold requirement is fulfilled if the test is good and the analysis convincing. Validation may include: preferably experiments, informatics analysis (complexity, run time) of an algorithm, or user studies.**

To find out whether Easy BBK is a user-friendly software which can help people with search biobricks of good quality and present their bio-systems. We have contacted 9 members of SJTU-bioX-Shanghai and members of SUSTC-Shenzhen to conduct user studies. More detailed information of user studies are available here:

<http://2014.igem.org/Team:SJTU-Software/Project/UserStudy>.

And the second goal can be any one of the following:

### **1. Make your software interact / interface with the Registry.**

Users can access the main page of the biobrick from “Search”. Additionally, biobricks can be uploaded to Registry. User guide is available through this page:  
<http://2014.igem.org/Team:SJTU-Software/Project/Tutorial>.

### **2. Re-use and further develop previous iGEM software projects (or parts thereof) or use and/or improvement of existing synthetic biology tools or frameworks.**

The assessment model is further developed from the attributes used to assess the biobricks used by 2012 UT-Tokyo-Software. Description of their attributes are available through this link: <http://2012.igem.org/Team:UT-Tokyo-Software/Project/BioBrickSearch>. Description of attributes used to assess the biobricks are available through this link: <http://2014.igem.org/Team:SJTU-Software/Database/AssessmentModel>.

### **3. Develop a well documented library or API for other developers (rather than “only” a stand-alone app for end users.)**

A well documented API documentation was automatically built from source code documentation using doxygen. Download of this documentation is available through this link: <http://2014.igem.org/Team:SJTU-Software/Database/FutureDevelopment>.

### **4. iGEM projects involve important questions beyond the bench, for example relating to (but not limited to) ethics, sustainability, social justice, safety, security, or intellectual property rights. Describe an approach that your team used to address at least one of these questions. Evaluate your approach, including whether it allowed you to answer your question(s), how it influenced the team’s scientific project, and how it might be adapted for others to use (within and beyond iGEM). We encourage thoughtful and creative approaches, and those that draw on past Policy & Practice (formerly Human Practices) activities.**

We have encountered two safety problems during the development of our software. The first one is the safety of our server. We have once accidentally upload user name and password of the server to GitHub without notice. Then we have changed the password to get access to the server. Later, we planned not to upload the file which contained the user name and password of server, but we will still compile the file in the executable file. Other users and developers won’t get access to this. The second one is with the username and password of the users who want to upload biobricks to Registry. We process this in a special way so that the username and password will not be saved locally or anywhere.

## **4.2 Acknowledgement**

As the first software team in Shanghai Jiao Tong University, we couldn’t have gone so far without the help of the instructors and decision makers in our university.

Here we extend great thanks to the School of Life Science and Biotechnology and School of Electronic Information and Electrical Engineering in SJTU.

Especially, we are quite grateful to the instructors who have always supported us during the whole project. They are Dr. Chaochun Wei, Dr. Hongyu Ou, Dr. Feng Chen and Dr. Guangyu Yang.

We also thank the team SUSTC-Shenzhen and SJTU-biox-Shanghai for providing us with detailed feedbacks on our software.

## **5 TEAM**

### **5.1 Member**

Jiabei Yang is the team leader of SJTU-Software. She is a senior student who majors in bioinformatics and biostatistics in school of life science and biotechnology.

As the first team leader of software team in SJTU, she made contacts with teachers in school to get support at the beginning of the project. She built up the team and recruited most members of team. She has kept a close eye on the development of the project, and is responsible for database construction and the establishment of biobrick assessment model. She wrote most of the document of the project.

Yibai Chen is the last programmer to join us yet he is the most important designer of Easy BBK. He is a senior student majoring in bioengineering in school of life science and biotechnology.

Although he majored in bioengineering, he studies computer science as his second major. He wrote the whole background program of Easy BBK and API documentation. Also, he communicate well with all those on our team who wrote GUI to connect the interface with data center and demonstrate ability to cooperate with others.

Sinan Lai is the only graduate student on the team majoring in communicating engineering. He is responsible for GUI of “search”, “compare” and “upload” page. It was really a big contribution.

As the only senior in team, he set a model for us, that is, throughout the summer vacation, he was always the first one to attend our discussion meeting and the last one to leave.

Chang Liu takes the responsibility of composing GUI of the “present” page and connecting with data center composed by Yibai Chen. He is a junior student majoring in biomedical engineering. Moreover, he is talented in communicating with others. Chang Liu has kept a good relationship with other teams and it has turned out that he has done a great job.

Wei Cao is mainly responsible for the maintenance of database. He is a senior student who majors in bioinformatics and biostatistics in school of life science and biotechnology.

Thanks to his bioinformatics background, he cooperate well with Jiabei Yang and Jingzhi Pang to set up the Easy BBK database and assessment model.

Weijian Cao composed the background program of upload. He is a senior student majoring in electronic information engineering in school of electronics information and electrical engineering.

He has a great sense of humor. Working with him is quite enjoyable. What’s more, he is talented in video edit and photoshop.

Jianhua Han is responsible for our team’s wiki. He is the youngest member on SJTU-Software and he is a junior student majoring in computer science in School of Electronics Information and Electrical Engineering.

He’s really a cute boy and hard-working. The final wiki’s source code was mainly composed by him.

Jingzhi Pang is responsible for the application of “Blastn” function and do pre-research work for our project. She is a senior student who majors in bioinformatics and biostatistics in school of life science and biotechnology.

As one of the first team members on team, she made great contributions to establishing contacts with teachers and professors in our university. She enjoys working with other members on



SJTU-Software.

Yeting Wu is the art designer on our team who joined us at the last minute. She is a sophomore majoring in communications from school of media and design.

She designed everything related to our team including the interface of the software, wiki of our wiki, banner, poster and so on. It was quite lucky for our team to have her as a team member.

Yue Wu took responsibility of part of GUI of Easy BBK. She is a senior student majoring in automation in School of Electronics Information and Electrical Engineering.